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AMENDMENT
Docket No. GP091-02.UT

Amendments to the specification:

Please make the following changes to pages 13 and 48.

At page 13, lines 2-15:

412
FIG. 2 shows the 5' to 3' DNA base sequence (SEQ ID NO:24) of the region surrounding the *bcr-abl* splice junction, as shown schematically in FIG. 1A, where the underlined region (residues 1 to 126) represents the *bcr* b2 sequence containing the sequence complementary to a primer binding site (bolded residues 65 to 88, SEQ ID NO:5) and the sequence complementary to the b2 probe binding site (bolded and italicized residues 89 to 113, SEQ ID NO:9); the double underlined region (residues 127 to 201) represents the *bcr* b3 sequence; the splice junction occurs between bases 201 and 202 and the remaining sequence is the A2 region of *abl* containing the *abl* primer binding site (bolded, SEQ ID NO:22).

FIG. 3 shows the 5' to 3' DNA base sequence (SEQ ID NO:25) of the region surrounding a potential splice junction in a normal *abl* transcript where: residues 1 to 151 are *abl* 1b exon sequence containing a region complementary to an *abl* primer binding site (residues 84-103, bolded, SEQ ID NO:13); the double-underlined region (residues 102 to 119, SEQ ID NO:26) is the complement of an *abl*-specific probe binding site flanking the splice junction of *abl* b1 and *abl* b2; the underlined region (residues 142 to 165, SEQ ID NO:16) is the complement of second probe binding site that overlaps potential splice junctions; and residues 175 to 201 (bolded, SEQ ID NO:22) are normal *abl* sequence containing another primer binding site.

At page 48, lines 5-8:

413
~~A simplified method for preparing nucleic acid, preferably spliced mRNA, from a biological sample that is suitable for amplification is disclosed. The invention includes methods A method of detecting and measuring the amount of one or more species of *bcr-abl* spliced mRNA present in the sample, following nucleic acid amplification, is disclosed.~~